

SEQUENCE LISTING

<110> Genentech, Inc.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
 35 40 45

Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
 65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
 115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
 130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
 145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
 165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
 180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
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Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115	120	125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165	170	175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180	185	190	
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195	200	205	
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210	215	220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245	250	255	
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260	265	270	
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275	280	285	
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
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Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
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His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
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Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
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Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 7
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<210> 8
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 9
<211> 22
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<212> DNA
<213> Artificial Sequence

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<210> 11
<211> 2197
<212> DNA
<213> Homo sapiens

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<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
 85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
 130 135 140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
 145 150 155 160

His Asp Pro Gly

<210> 13
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 <213> Homo sapiens

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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 35 40 45
 Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60
 Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80
 Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95
 Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110
 Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125
 Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140
 Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160
 Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175
 Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 20
 tgcacaaggc ggtgtcacag cacg 24

<210> 21
 <211> 44
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 21
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<210> 22
 <211> 1200
 <212> DNA
 <213> Homo sapiens
 <400> 22
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<210> 23
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 23

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			20				25					30			

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
				35				40				45			

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
				50			55				60				

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
				65			70			75			80		

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
				85				90				95			

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
				100				105				110			

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Glu	Asn	Asn	Tyr	Thr
				115			120				125			

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
				130			135				140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
				145			150			155		160			

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
				165				170				175			

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
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Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr		
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<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtaacgtga gggaccaggg cgccatga

28

<210> 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccgggtgacct gcacgtgctt gccaa                                         24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t                                         41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggaggtc tggacttcaa cagaacccca 180
tccagtcatt ttgattttgc tggttatttt ttttttctt ttcttttcc caccacattg 240
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tcctggcctg ccctagtgtg tgccgcgtcg acaggaactt tgtctactgt aatgagcgaa 420
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atctgatcag gctctatttgc caggacaacc agataaaacca cattccttgc acagccttct 1080
caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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 taaatatgaa tctttgtcc tgtcccacca cgaccccccgg cctgcctctc ttcaccagg 1380
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 gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactggatg 1500
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 ttgtgctggt ggtcttgctc agcgtcttt gctggcatat gcacaaaaag gggcgctaca 1980
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
 50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
 85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
 100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 29
cggtctacct gtagggcaac c                                21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 30
gcaggacaac cagataaaacc ac                                22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc                                22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac      46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
acttgagca agcggcggcg gcgagacag aggcagaggc agaagctggg gctccgtcct 60
cgcctccac gagcgttccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

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<210> 34
 <211> 915
 <212> PRT
 <213> Homo sapiens

<400> 34
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245	250	255	
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265	270	
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280	285	
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295	300	
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330	335	
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345	350	
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360	365	
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410	415	
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425	430	
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440	445	
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490	495	
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505	510	

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

Arg Tyr Arg
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36

acagccatgg tctatacgctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 37
 gcctgtcagt gtcctgaggg acaacgtgctc cgcagcgtatg ggaag 45

<210> 38
 <211> 1813
 <212> DNA
 <213> Homo sapiens

<400> 38
 ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcagcct 60
 cggcacctgc aggtccgtgc gtcccgccgc tggccgcctt gactccgtcc cggccaggga 120
 gggccatgtat ttccctcccg gggcccttgg tgaccaactt gctgcgtt ttgttcttgg 180
 ggctgagtgc cctcgccccc ccctcgccggg cccagctgca actgcacttg cccgcacaacc 240
 ggttgcaggc ggtggaggga gggaaagtgg tgcttccagc gtggtacacc ttgcacgggg 300
 aggtgtcttc atccccagcca tgggaggtgc cctttgtat gtggttcttc aaacagaaaag 360
 aaaaggagga tcaggtgttgc tcctacatca atggggtac aacaagcaaa cctggagttat 420
 ccttggtcta ctccatgccc tccccgaacc tgccctgtcg gctggagggt ctccaggaga 480
 aagactctgg cccctacagc tgctccgtga atgtcaaga caaacaaggc aaatctaggg 540
 gccacagcat caaaacctta gaactcaatg tactggtcc tccagctctt ccattctgcc 600
 gtctccaggc tggcccccattt gttggggcaa acgtgacccct gagctgcccag tctccaaggaa 660
 gtaagccgc tggccaataac cagttggatc ggcagcttcc atccttccag actttcttg 720
 caccagcattt agatgtcatc cgtgggtctt taaggctcac caacctttcg tcttccatgg 780
 ctggagtcata tggctgtcaag gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
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 ttggacttggg gttgtggctt gggctggtcc tcttgtacca ccggccgggc aaggccctgg 960
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 aaggatttgg ggtctcttc tccatataagg gtcacccatca gcacagaggg ctgagtcatg 1380
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 attggagggaa gcctccaccc acccccttgcactt cctcccttgc aagccagctg ctgaaatttag 1560
 ctactcacca agagtggggaa gcagagactt ccagtacttgc agtctcccttgc gcccccttgc 1620
 tctgtacccccc accccctatctt aacaccaccc ttggctccca ctcagctcc ctgtattttat 1680
 ataacactgtc aggctggctt ggtaggttt tactggggca gaggataggg aatctcttat 1740
 taaaactaac atgaaatatgt tggatgttttgc atttgcataat ttaataaaatg atacataatg 1800
 tttgtatgaa aaa 1813

<210> 39
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15												
Phe	Leu	Gly	Leu	Ser	Ala	Leu	Ala	Pro	Pro	Ser	Arg	Ala	Gln	Leu	Gln
	20					25						30			
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val
	35					40						45			
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln
	50					55						60			
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys
	65				70				75			80			
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro
					85				90			95			
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg
					100				105			110			
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val
	115					120						125			
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr
	130					135						140			
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu
	145				150				155			160			
Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser
					165				170			175			
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro
					180				185			190			
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser
						195			200			205			
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys
					210				215			220			
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu
					225				230			235			240
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly
					245				250			255			
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His
					260				265			270			
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp
					275				280			285			

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttaa 2220
 atcagtttt ctgttatgc tataggact gtagataata aggtaaaatt atgtatcata 2280
 tagatatact atgttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
 ggaaagtaat tggttctca ggagtatat cactgcaccc aaggaaagat tttctttcta 2400
 acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatattc tgtgactcgt 2460
 gttgccttg aaactagtc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
 cataagagaa tgaaggggca gaatatcaa cagtgaaaag ggaatgataa gatgtattt 2580
 gaatgaactg tttttctgt agactagctg agaaattgtt gacataaaat aaagaattga 2640
 agaaaacacat tttaccattt tgtgaattgt tctgaactt aatgtccact aaaacaactt 2700
 agacttctgt ttgctaaatc tggttcttt tctaataattc taaaaaaaaaaa 2760
 acctccacaa attgaa 2820
 aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1 5 10 15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
 20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
 35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
 50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
 65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
 85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
 100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
 115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
 130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
 145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
 165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190	
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val			
195	200	205	
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys			
210	215	220	
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe			
225	230	235	240
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys			
245	250	255	
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met			
260	265	270	
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala			
275	280	285	
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser			
290	295	300	
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln			
305	310	315	320
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile			
325	330	335	
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys			
340	345	350	
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser			
355	360	365	
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp			
370	375	380	
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser			
385	390	395	400
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly			
405	410	415	
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln			
420	425	430	
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr			
435	440	445	
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys			
450	455	460	

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

tggaaacata tcctccctca tatgaatatg gatggagact acataaaat atttccaaag 60
 ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcatttttta tattataaga 120
 gtattggtcc ctttgcttcc atcatctgac aacttcttat tgaaacctca aaattatgat 180
 aattctgaag aggagggaaag agtcataatct tcaagtaattt cagtcataat gagctcaa 240
 ccaccacat tataatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
 gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
 tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacaccc 420
 aatcacctga cacatttgc aattttgatg tcctctggc cttcatttgg tattaaagat 480
 tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540
 atatgcattt ttaccttctg gtttttcagt gaaattcaaa gcaccaggaa 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgataac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
ggatctcctg agctcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
cctagttgag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgttaatc acctgacaca ttttgcatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
gctcccgagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaaccggc 60
cgctaaggcgaa ggcctctcc tcccccgat ccgaacggcc tggggcgqqqt cacccccqqct 120

gggacaagaa gccggcgct gcctgccccg gccccgggag ggggctgggg ctggggccgg 180
 aggcggggtg tgagtgggtg tgcgggggg gcgaggctt gatcaatcc cgataagaaa 240
 tgctcggtg tcttgggcac ctaccgtgg gccccgttaag gcgctactat ataaggctgc 300
 cggcccgag ccggccgcgc gtcagagcag gagcgcgtcg tccaggatct agggccacga 360
 ccatcccaac ccggcactca cagccccca ggcgcattccg gtgcggccgc agcctccgc 420
 accccatcg ccggagctgc gccgagagcc ccagggaggt gccatgcgga gcggtgtgt 480
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 cttctcgac gccccggccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
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 cagtgccaa cagcggcagc tgtacaagaa cagaggctt cttccactct ctcatttct 960
 gcccatgctg cccatggtcc cagaggagcc tgaggaccc agggccact tggaatctga 1020
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 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgccccgg gcctcttcac 1140
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 aaaattctta tgtcaagctg aaattctcta atttttctc atcaactccc caggagcagc 1500
 cagaagacag gcagtagttt taatttcagg aacaggtat ccactctgtaa aacacagcagg 1560
 taaatttcac tcaaccccat gtggaaattt atctatatct ctacttccag ggaccatttg 1620
 cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
 ggagtagggg aaggctggag ccccaactcca gcccctggac aacttgagaa ttccccctga 1740
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 ccatctccca gcccaccagc cctctgccc ctcacatgc ctcccatgg attggggcct 1860
 cccaggcccc ccacctttagt tcaacctgca ttcttgc aaaaatcagg aaaagaaaaag 1920
 atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacacta 1980
 gaacccttc cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040
 tgtacatctc ttatttctt acattattta tgcccccaa ttatattt gtatgttaagt 2100
 gaggttggtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
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Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
			20					25				30			

His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
			35					40				45			

Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
			50			55			60						

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60
 atccggccag atggctacaa tgtgtta 26

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61
 gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtcgggt gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caagggccccc cggcctcctg cgctcctgcc gcccggaccc tcgacccct 60
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120
 gctgctgctg cgctacctgg tggtcgcctt gggctatcat aaggcctatg ggtttctgc 180
 cccaaaagac caacaagttag tcacagcagt agagtaccaa gaggttattt tagcctgcaa 240
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300
 ctgttctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360
 tttcaatatac cggatcaaaa atgtgacaag aagtgtatgcg gggaaatatac gttgtgaagt 420
 tagtgccca tctgagcaag gccaaaacctt ggaagaggat acagtcactc tggaaagtatt 480
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtgg 540
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 acccgggagg cggaggttgc agttagctga gatcacgcctt ctgcagttcc gcctgggtaa 1200
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 65
 atcggttga agtttagtgcc cc 22

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 66
 acctgcgata tccaaacagaa ttg 23

<210> 67
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 67
 ggaagaggat acagtcaactc tggaaagtatt agtggctcca gcagttcc 48

<210> 68
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 68
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 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gtcacagc ccggaccctg 120
 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaataa ttacttct 180
 aaataaaatga attactcaat ctcctatgac catctataaca tactccaccc tcaaaaagta 240
 catcaaatatt atatcattaa gaaaaatgtt accttctt ctcataatg catgacattt 300
 ttggacaatgtt caattgtggc actggactt atttcgttga agaaaaactt ttttttttctta 360
 tggcattcat catttgcacaa atgcaagcat cttccttatac aatcagctcc tatttgcactt 420
 actagcaactg actgtggat ctttaagggc cattacatt tctgaagaag aaagctaaga 480
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540

aagctgtaga taaaaaaagtg gattgtccac gtttatgtac gtgtgaaatc aggccttgg 600
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 taggttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
 1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350	
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn			
355	360	365	
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr			
370	375	380	
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro			
385	390	395	400
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met			
405	410	415	
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu			
420	425	430	
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala			
435	440	445	
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu			
450	455	460	
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr			
465	470	475	480
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys			
485	490	495	
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys			
500	505	510	
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys			
515	520	525	
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser			
530	535	540	
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr			
545	550	555	560
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys			
565	570	575	
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys			
580	585	590	
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn			
595	600	605	
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn			
610	615	620	

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
 625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
 645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
 690 695 700

Thr Asn Met Ser
 705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

gccccggact ggcgcaagg gccaagcaa ggaaagaaaat aatgaagaga cacatgttt 60
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 ttaccacgct tggatggat gatgaggaat gggctcgta ttatgctgac attccagcat 180
 gaatctgttta gacctgtggta taacccttc cctctccatg tgcgttccctcc tacaaaagtt 240
 tggatctttagt atactgtgct ttcattctgc cagttatgtt cccaaaggct gtctttgtc 300
 ttccctctggg ggtttaaatg tcacctgttag caatgcataat ctcaaggaaa tacctagaga 360
 tcttccttcctt gaaacagtct tactgtatct ggactccat cagatcacat ctattcccaa 420
 tgaaaatttt aaggacctcc atcaactgtag agttctcaac ctgtccaaaa atggcattga 480
 gtttatcgat gacatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
 cgacaatcggtt attcaaaatgt tgccatgttgc tgcataat aacctgaaagg ccaggccag 600
 aattgccaac aacccctggc actgcgactg tactctacag caagtctgaa ggagcatggc 660
 gtccaaatcat gagacagcccc acaacgtgat ctgtaaaacg tccgttgg atgaacatgc 720
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 cttaactttt aaccatggaa aaaaaaaaaaaa aaaaaaaaaaa aaaca 1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Gly Gly Leu Asn Val
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255

Thr Val Val

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> *Homo sapiens*

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile	610	615
		620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 74

tcacacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75

ataccaggcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg
gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77	
ccatgtgtct ctcctacaa ag	22
<210> 78	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 78	
ggaaatagat gtgatctgat tgg	23
<210> 79	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 79	
cacctgttagc aatgcaaatc tcaaggaaat accttagagat cttcctcctg	50
<210> 80	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 80	
agcaaccggcc tgaagctcat cc	22
<210> 81	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 81	
aaggcgccggt gaaaagatgt a gacg	24
<210> 82	

<211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
 cccacgcgtc cgcacacctgg ccccggtc cgaagcggtc cggggggcgcc ctttcggta 60
 acatcgtagt ccacccccc cccatccccca gccccccgggg attcaggctc gccagcgccc 120
 agccaggag cccggccggga agcgcgtatgg gggccccagc cgcctcgctc ctgctcctgc 180
 tcctgtgtt cgcctgtgtc tggggccccg gggggccaa cctctccag gacgacagcc 240
 agetcctggac atctgtatgaa acagtgggtt ctgggtggcac cgtgggtgtc aagtgcctaaag 300
 tgaaagatca cgaggactca tccctgtcaat ggtctaaccct tgctcagcag actctctact 360
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagttac acctgtctaa 480
 tcttcactat gcctgtgtc actgccaatg ccctcgtaac tgtgttagga attccacaga 540
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 ccctttccgt ggcttctctg catttgggtt attattattt ttgtacaat cccaaatcaa 1620
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
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Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87		
cctagcacag tgacgaggga cttggc		26
<210> 88		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 88		
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc		50
<210> 89		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 89		
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<210> 90		
<211> 2755		
<212> DNA		
<213> Homo sapiens		
<400> 90		
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cagactgcag ggttaaagacc tcaatgaaac caccgaacag gacttgc 960		
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cctgccaact ctttcaaga caaatggca agaggatcat gccacaccag ggtctgc 1080		

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 caggtggcta tacatggata gcaattaccc ggacacgcgt tccgggaga aattcgcggg 1500
 gtcgaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctccggg 1560
 cacttcaat gccatgccc aactgaggat cctcattctc aacaacaacc tgctgagtc 1620
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 gcacaaccga aaggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
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Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Gly Phe Thr
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95

Ile	Val	Pro	Gly	Ala	Phe	Leu	Gly	Leu	Gln	Leu	Val	Lys	Arg	Leu	His
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Ile	Asn	Asn	Asn	Lys	Ile	Lys	Ser	Phe	Arg	Lys	Gln	Thr	Phe	Leu	Gly
115								120					125		
Leu	Asp	Asp	Leu	Glu	Tyr	Leu	Gln	Ala	Asp	Phe	Asn	Leu	Leu	Arg	Asp
130								135					140		
Ile	Asp	Pro	Gly	Ala	Phe	Gln	Asp	Leu	Asn	Lys	Leu	Glu	Val	Leu	Ile
145								150				155			160
Leu	Asn	Asp	Asn	Leu	Ile	Ser	Thr	Leu	Pro	Ala	Asn	Val	Phe	Gln	Tyr
165								170					175		
Val	Pro	Ile	Thr	His	Leu	Asp	Leu	Arg	Gly	Asn	Arg	Leu	Lys	Thr	Leu
180								185					190		
Pro	Tyr	Glu	Glu	Val	Leu	Glu	Gln	Ile	Pro	Gly	Ile	Ala	Glu	Ile	Leu
195								200					205		
Leu	Glu	Asp	Asn	Pro	Trp	Asp	Cys	Thr	Cys	Asp	Leu	Leu	Ser	Leu	Lys
210								215					220		
Glu	Trp	Leu	Glu	Asn	Ile	Pro	Lys	Asn	Ala	Leu	Ile	Gly	Arg	Val	Val
225								230				235			240
Cys	Glu	Ala	Pro	Thr	Arg	Leu	Gln	Gly	Lys	Asp	Leu	Asn	Glu	Thr	Thr
245								250					255		
Glu	Gln	Asp	Leu	Cys	Pro	Leu	Lys	Asn	Arg	Val	Asp	Ser	Ser	Leu	Pro
260								265					270		
Ala	Pro	Pro	Ala	Gln	Glu	Glu	Thr	Phe	Ala	Pro	Gly	Pro	Leu	Pro	Thr
275								280					285		
Pro	Phe	Lys	Thr	Asn	Gly	Gln	Glu	Asp	His	Ala	Thr	Pro	Gly	Ser	Ala
290								295					300		
Pro	Asn	Gly	Gly	Thr	Lys	Ile	Pro	Gly	Asn	Trp	Gln	Ile	Lys	Ile	Arg
305								310				315			320
Pro	Thr	Ala	Ala	Ile	Ala	Thr	Gly	Ser	Ser	Arg	Asn	Lys	Pro	Leu	Ala
325								330					335		
Asn	Ser	Leu	Pro	Cys	Pro	Gly	Gly	Cys	Ser	Cys	Asp	His	Ile	Pro	Gly
340								345					350		
Ser	Gly	Leu	Lys	Met	Asn	Cys	Asn	Asn	Arg	Asn	Val	Ser	Ser	Leu	Ala
355								360					365		
Asp	Leu	Lys	Pro	Lys	Leu	Ser	Asn	Val	Gln	Glu	Leu	Phe	Leu	Arg	Asp
370								375					380		

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp
 690 695

<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
 gttggatctg ggcaacaata ac

22

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgttgtgc aggctgagtt taag

24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
 ggtggctata catggatagc aattacctgg acacgctgtc ccgggg

45

<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95
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gaggggaaagg gagggggaaac cgggttgggg aagccagctg tagagggcgg tgaccgcgt 240
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tgggcactcc tttttttttt tgatgaaaacg gggaaaccaag aggaacttac 1860
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aggatgggtga tactggggga ccgggttagtg ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgtat tgaactttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctacccaaa atggaaaggg aatgttctat gttgttcagg 2160
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gttqat 2226

<210> 96

<211> 490

<212> PRT

<213> *Homo sapiens*

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 97
 tggaaggaga tgcgatgcca cctg

<210> 98
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 98
 tgaccagtgg ggaaggacag

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<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 99
acagagcaga gggtgccattg                                         20

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 100
tcagggacaa gtgggtgtctc tccc                                         24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 101
tcagggaaagg agtgtgcagt tctg                                         24

<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 102
acagctcccg atctcagtta cttgcattgc ggacgaaatc ggcgctcgct          50

<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens

```

<400> 103

ggacgcgcgtg ggattcagca gtggcctgtg gctgccagag cagctctca ggggaaacta 60
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tatcccccg ctacctggc cggcccgcc cggtgcgcgc gtgagaggga ggcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtgtgc ggcagtgtga gggccgtgt gagcgcgggtg 240
ggtgcggagg ggcgtgtgtg cggcgcgcg cggcgtgggg tgcaaacccc gacgtctac 300
gctgccatga gggcgcgaa cgcctggcg coactctgc tgctgtgg tgccgcacc 360
cagctctcgc ggcagcagtc cccagagaga ctgtttca catgtgttgg cattctact 420
ggagagtcg gatttattgg cagtgaaggt ttctctggag tgtaccctcc aaatagcaa 480
tgtacttggaa aaatcacagt tccgaagga aaagtagtgc ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgcgcctat gactttgtgg atgttacaa tggccatgcc 600
aatggccagc gcattggcg ttctgtggc actttccggc ctggagccct tgggtccagt 660
ggcaacaaga ttaggtgcgatgatttct gatgccaaca cagctggcaa tgggttcatg 720
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gacagacett ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
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gtgttatttgc tttcaccttca aagccttgc cctgaggtgt tacaatcttgc tcttgcgtt 1980
tctaaatcaa tqcttaataa aatattttta aqgaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340

345

350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
 355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
 385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
 405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

<210> 109

<211> 420

<212> PRT

<213> *Homo sapiens*

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
 20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
 35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
 50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgta

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgttgt agccctcgac ac

22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113

tgagaccctc ctgcagcctt ctcaaggac agccccactc tgcctttgc tcctccaggg 60
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 cggggccgccc ctgaccgggg agcagctctt gggcagcctg ctgcggcagc tgcagctcaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatccca cccacgtgag 240
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttctggcg ttggaggcca gcacacacac 360
 gctggtgttc ggcattggagc agcggctgcc gccaaacagc gagctgtgc aggccgtgt 420
 gccggctcttc caggagccgg tccccaaaggc cgccgtgcac aggacccggc ggctgtcccc 480
 gecgcagcgcc cgggccccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540
 cccgacccctcc ctcatcgact ccaggctggt gtccgtccac gagagccggct gaaaggccctt 600
 cgacgtgacc gaggccgtga acttctggca gcagctgagg cggcccccggc agccgctgt 660
 gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcttcggcg cccacaagat 720
 ggtccgcgtt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
 caccctggac ctgggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
 cgagaactgg gtgctggagc ccccggtt cttggcttat gagtgtgtgg gcacctgcg 960
 gcagcccccg gaggccctgg cttcaagtgc gcccgttctg gggcctcgac agtgcacgc 1020
 ctccggagact gactcgctgc ccatgatcgat cagcatcaag gagggaggca gacccaggcc 1080
 ccaggtggtc agcctgccc acatgagggt gcaagaatgc agctgtgcct cggatggtc 1140
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 ggacaaatgc tctgtctctt ctatgtgaccc ctgaatttgc ttccctgtac aagttaccc 1320
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 aaagtccctcc accaccactc tggacctaag acctgggtt aagtgtgggt tgcaccc 1560
 caatccagat aataaaagact ttgtaaaaca tgaataaaaac acattttattt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114

Met	Gln	Pro	Leu	Trp	Leu	Cys	Trp	Ala	Leu	Trp	Val	Leu	Pro	Leu	Ala
1															

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgccaaacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggaggtaaaggcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggtgt tgtgtcagtgcgcctgatcgc gatggggaca 60
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 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatccgtgtga agttgtcctg tgcctactcg ggctttctt ctccccgtgt ggagtggaaag 240
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 gaggaccggg tgaccttctt gcacaactggt atcaccttca agtccgtgac acgggaagac 360
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 agctgctcag gggctggca acaagagcaa aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295
 <210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 120
 tcgcggagct gtgttctgtt tccc 24
 <210> 121
 <211> 50

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaagctc gagagggaaac tgggtgtgcct      50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 122
acacacctggtt caaagatggg      20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg      24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 124
ttgccttact caggtgctac      20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```

oligonucleotide probe

<400> 125
 actcagcagt ggttaggaaag 20

<210> 126
 <211> 1210
 <212> DNA
 <213> Homo sapiens

<400> 126
 cagcgcgtgg ccggcgccgc tggggaca gcatgagcgg cggttggatg gcgagggtg 60
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgt gctgctggc ctcggactag 120
 gcctggaggc cgccgcgagc cccgtttcca cccgaccc tcggcaggcc gcaggcccc 180
 gtcagggtc gtgcccaccc accaagtcc agtgcgcac cagttggctt tgctgtcccc 240
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
 ggattgagcc atgtacccag aaaggcaat gcccacccgc ccctggcctc ccctgcccct 360
 gcacccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcacac tgcagccccc 420
 tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
 ggcgcgtgcga cggccaccca gactgtcccg actccagcga cgagctggc tggaaacca 540
 atgagatcct cccggaagg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600
 tcacctctct caggaatgcc acaaccatgg ggcccccgtt gaccctggag agtgcctccct 660
 ctgtcgggaa tgccacatcc tcctctggcg gagaccagtc tggaagccca actgcctatg 720
 gggttattgc agctgctgcg gtgctcagt gcaaggctgtt caccgcacc ccctccctt 780
 tgtcctggct ccgagcccgag gagegcctcc gcccactggg gttactggtg gcatgaagg 840
 agtccctgtc gctgtcagaa cagaagaccc cgctgcctg aggacaagca cttgcccacca 900
 ccgtcaactca gcccctggcg tagccggaca ggaggagagc agtgcgtggc atgggtaccc 960
 gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaaccc gaacccgagc 1020
 tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
 agcttaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctccctg 1140
 gggtagaaac gcccctgtgc ttaagacact ccctgctgccc cctgctgagg gtggcgattta 1200
 aagttgcttc 1210

<210> 127
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280
 <210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 128
 aagttccagt gccgcaccag tggc
 <210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

 <400> 131
 cccacgcgtc cggctctcgct cgctcgca gcggcgccag cagaggtcgc gcacagatgc 60
 gggttagact ggcgggggga ggaggcgag gagggaagga agctgcattgc atgagaccca 120
 cagactcttgc caagctggat gccccttgc gatgaaagat gtatcatggat atgaaccgaa 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcgc tggcgctgtg cttccggccct gcacagctca 300
 cgggcgggtt cgatgacccctt caagtgtgtg ctgaccccgat cattcccgag aatggcttca 360
 ggaccccccag cggagggggtt ttcttgaag gctctgtgc ccgatttcac tgccaagacgc 420
 gattcaagct gaaggggcgct acaaagagac tggatgttgc gcatatataat ggaacccttag 480
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgcgtatc cctcaaatacg 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgc 600
 atgaaggatt caagatccgg taccggacc tacacaatat ggtttcattt tgtcgcgtatc 660
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
 atggctatgt aaacatcttctt gagctccaga cctccttccc ggtggggact gtatcttctt 780
 atcgctgtt tccccggatt aaacttgcgtt ggtctgcgtt tcttgcgttgc ttacaaaacc 840
 ttatctggtc gtccagccca ccccggtgcc ttgtctgttgc agcccaagtc tggccactac 900
 ctccaaatgtt gagtcacggat gatttcgttgc gccacccgcg gcctgttgc gctacaacc 960
 acggaactgt ggtggagttt tactgcgtt cttggctacag cttcaccaggc gactacaatgt 1020
 acatcacctg ccagtatggat ggtgttttgc cttcttataca agtctactgc atcaaatacg 1080
 agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcggttca 1140

cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
 agttcaaggc ccacttccc cccagggggc ctcccccggag ttccagcagt gaccctgact 1260
 ttgtgggtt agacggcgtg cccgtcatgc tcccgccata tgacgaagct gtgagtgccg 1320
 gcttggatgc cttaggcccc gggatcatgg cctctgtggg ccaggcgtgc cccttacccg 1380
 tggacgacca gagcccccca gcatacccg gctcagggga cacggacaca ggcccagggg 1440
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
 ctccccagggtg ccaagagagc acccaccctg cttcgacaa ccctgacata attgcccagca 1560
 cggcagagga ggtggcatcc accagccag gcatccatca tgcccaactgg gtgttgc 1620
 taagaaactg attgattaaa aaatttccca aagtgtccctg aagtgtctt tcaaatacat 1680
 gttgatctgt ggagttgatt ccttccttc tcttggttt agacaaatgt aaacaaagct 1740
 ctgatcctta aaattgctat gctgatagag tggtagggc tggaagctt atcaagtcct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1 5 10 15

Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgcttcc cg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccggt cggtccgtcg gtggcctaga 60
 gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtccggc catgaggccg ggaaccgcgc 180
 tacagggcgt gctgctggc gtgctgctgg tggggctgctg ggcgcgcacg ggtcgccctgc 240
 ttagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccggga gggacacacaga 300

ggccttgtta taaagtatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtca gatcgagtct gaagatgaac 420
 agaaaactgat agaaaagtcc attgaaaacc tcttgcattc tgatggatc ttctggattt 480
 ggctcaggag gcgtgaggag aaacaaaagca atagcacagc ctgcaggac ctttatgct 540
 ggactgatgg cagcatatca caatttaga actggatgtt gcatggccg tcctgcgc 600
 gcgaggtctg cgtggatcatg taccatcagc catcgccacc cgctggatc ggaggccc 660
 acatgttcca gtggatgtt gaccggcgtca acatgaagaa caatttattt tgcaaataatt 720
 ctgatgagaa accagcaggc cttcttagag aagctgaagg tgaggaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacattt aaagaaagta 840
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctcctcc 900
 ttgtgtcac cacagtgtt tggtgggtt ggtatctgtt aaaaagaaaa cgggagcagc 960
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaaacagcc 1020
 cggacccatg ggtctacaat gtcataagaa aacaaagcga agctgactt gctgagaccc 1080
 ggcagacccatg gaagaatatt tcattccgag tggatgttccgg agaagccact cccgatgaca 1140
 tggatgttca ctatgacaac atggatgtt gacccatcaga aagtgggtt gtgactctgg 1200
 tgagcgttca gaggatgtt gtgaccaatg acatttatgatg gttctccca gaccaatgg 1260
 ggaggatgaa ggaggatgtt ggggtggaaa atgaaatata tggatgttccgg gacatataaa 1320
 aaactgaaac tgacaacaat gggaaaagaaa tgataagcaa aatctcttta ttttctataa 1380
 gggaaaataca cagaaggctt atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
 tccccacgac ctcctgttgg acccccacgt tttggctgtt tccttctatcc cagccagtc 1500
 tccagctcga ctttatgaga aggtacccatg cccaggtctg gcacatagta gagtctcaat 1560
 aaatgtcaact tggatgttccgg tatcttactt ttaagggaca gagcttacc tggcagtgat 1620
 aaagatgggc tggatgttccgg gggaaaaccac ctctgttttc cttgtctat acagcagcac 1680
 atattatcat acagacagaaa aatccagaat ctttcaaaag cccacatatg gtagcacacagg 1740
 ttggctgttca catcgccaaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800
 agcaggaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
 100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aaccttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaagggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

 <400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgccg acttgggggc gcccgcgtgag ccccgccgc cgcagaagac 120
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tggtgtgttc agcatgcgt tttggacccc agtgggcgtc ctgacacgtcg tggcgtactg 240
 cctgcaccag cggcggttgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcggt tttcgacacg gggctcggag 360
 tcctctcaag cccgtcccgcc tggaggagca ggttagagtgg aaccccccagc tattagaggt 420
 cccaccccaa actcagtttgc attacacagt caccatcta gctgggtggc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540
 gctgaccaag gtgggcgtgc agcaaatttttgc tgccttggga gagagactga ggaagaacta 600
 tgtggaaagac attcccttgc tttcaccaac cttcaaccca caggaggtct ttattcggtt 660
 cactaacatt tttcgaaatc tggagtccac ccgttggc ctggctggc tttccagtg 720

tcagaaaagaa ggacccatca tcatccacac tcatcagaagca gattcagaag tcttgtatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
 tttacagcca ggaatctca aggattgaa aaaggtaag gacaggatgg gcattgacag 900
 tagtgataaa gtggacttct tcatttcctt ggacaacgtg gctggcgagc aggcacacaa 960
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcaacaga gagctgtgga 1020
 cacatcctt tacatactgc ccaaggaaga caggaaagt cttcagatgg cagtagggcc 1080
 attcctccac atccttagaga gcaacctgct gaaagccatg gactctgcca ctgccccgca 1140
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctttaat 1200
 gaccctgggg attttgacc acaaatggcc accgtttgtt gttgacactga ccatggaact 1260
 ttaccagcac ctggaatcta aggagtggtt tgcagctc tattaccacg ggaaggagca 1320
 ggtgccgaga gttgcccctg atggctctg cccgctggac atgttcttga atgccatgtc 1380
 agtttatacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
 agttgaaat gaagagtaac tgattataa aagcaggatg tggatgttt aaaataaagt 1500
 gccttataac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
 165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425
 <210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 143
 ccaactacca aagctgctgg agcc

<210> 144
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 144
 gcagctctat taccacggga agga

<210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 145
 tccttcccggt ggttaatagag ctgc

<210> 146
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 146
 ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg

<210> 147
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<400> 147
 ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
 cttaaatttc agtcatcac cttcacctgc cttggtcatg gctctgctat ttccttgat 120
 cttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtgg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
 gtgtatgac ggctggaca ttaaggacgt ggctgttgc tgccggagc tgggctgtgg 300
 agctgccagc ggaaccctta gtggatttt gtatgagcca ccagcagaaa aagagcaaaa 360
 ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
 agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccagg 480
 gagctttc tccccagttc cagagggtgt caggctggct gacggccctg ggcattgca 540
 gggacgcgtg gaagtgaagc accagaacca gtggatatacc gtgtgccaga caggctggag 600
 cctccggcc gcaaagggtgg tgcggccgc gctggatgt gggaggctg tactgactca 660
 aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
 ctcagacga gaagcaaccc ttcaaggattt cccttctggg ctttggggaa agaacactg 780
 caaccatgat gaagacacgt gggcgtaaatg tgaagatccc tttgacttga gacttagg 840
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 ggtggcattc atctaattctg ttgagtgctt gaatagaaga aaaacacaga agaaggagc 1200
 atttactgtc tacatgactg catggatgtg acactgatct tcttctgccc ttggacttggg 1260
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 tccacattgc acacagcaga ttcccagctt ccataattgt gtgtatcaac tacttaata 1440
 catttcaca cacacacacaca cacacacacaca cacacacacaca cacacataca ccatttgcc 1500
 tgtttctctg aagaactctg aaaaaataca gatttggta ctgaaagaga ttctagagga 1560
 acggaatttt aaggataaat ttctgaaattt ggttatgggg ttctgaaat tggctctata 1620
 atctaatttag atataaaaattt ctggtaactt tatttacaat aataaagata gcactatgt 1680
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149
 ttcagctcat caccttcacc tgcc 24
 <210> 150
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 150
 ggctcataca aaataccact aggg 24
 <210> 151
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 151
 gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50
 <210> 152
 <211> 1427
 <212> DNA
 <213> Homo sapiens
 <400> 152
 actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgaccccg 60
 acccacgcgt ccgccggacgc gtggggcggac gcgtggggccg gctaccagga agagtctgcc 120
 gaaggtgaag gccatggact tcacacccctc cacagccatc ctgcggccgc tggtcggtcg 180
 cctgggcgtc ttcggccctt tccggctgtc gcagtgggtg cgcgggaaagg cctacctgcg 240
 gaatgctgtg gtgggtgatca caggcgccac ctcagggctg ggcaaagaat gtgaaaagt 300
 ctctatgtc gcgggtgtca aactgggtgtc ctgtggccgg aatgggtgggg ccctagaaga 360
 gctcatcaga gaacttacccg ctctatgc caccaagggtg cagacacaca agccttaactt 420
 ggtgacccccc gacccacacag actctggggc catagttgca gcagcagctg agatcctgcg 480
 gtgcttggc tatgtcgaca tactgtcaa caatgtctggg atcagctacc gtggtaaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccaagt 600
 tgctctaaccg aaaggactcc tgcctccat gatcaagagg aggcaaggcc acattgtcg 660
 catcagcagc atccaggccca agatgagcat tcctttcga tcagcatatg cagcctccaa 720
 gcacgcaacc caggcttct ttgactgtct gcgtggccgg atggaaacagt atgaaattga 780
 ggtgaccccg atcagccccc gctacatcca caccaaccctc tctgttaatg ccatcaccgc 840
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 ggtggcccaag gatgttctg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgcct tccttggctg tttatctcg aactctgtct cctggctct tcctcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tccttagtact ctgaccagcc 1080

agggccaggg cagagaagca gcactcttag gtttgcttac tctacaaggg acagttgc 1140
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 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260
 ggaaacactt aaggaataaa tatggagctg ggtttaaca ctaaaaacta gaaataaaca 1320
 tctcaaacag taaaaaaaaaaa aaaaaaggc ggcgcgact cttagtcga cctgcagaag 1380
 cttggccgccc atggcccaac ttgttattt cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
 195 200 205

Glu Met Glu Gln Tyr Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156		
tcatactgtt ccatctcgac acgc		24
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 157		
aatgggggg ccctagaaga gctcatcaga gaactcacgg cttctcatgc		50
<210> 158		
<211> 1771		
<212> DNA		
<213> Homo sapiens		
<400> 158		
cccacgcgtc cgctgggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60		
aaaaaaaaaaa acacaccaaa cgctcgac cacaaaaggg atgaaattc ttctggacat 120		
cctccgtctt ctcgggttac tgatcgctg ctccctagag tccttcgtga agctttttat 180		
tcctaagagg agaaaatcg tcacccggcga aatcgctcg attacaggag ctgggcattgg 240		
aattggaga ctgactgcct atgaatttgc taaaacttaaa agcaagctgg ttctctggga 300		
tataaataag catggactgg agggaaacagc tgccaaatgc aaggactgg gtgccaaggt 360		
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420		
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480		
agattgttt gctacacaag atcctcagat taaaagact tttgaagtt atgtacttgc 540		
acatttctgg actacaaaagg catttcttcc tgcaatgac aagaataacc atggccatat 600		
tgtcaactgtg gcttcggcag ctggacatgt ctgggtcccc ttcttactgg cttactgttc 660		
aagcaagttt gctgtgttg gatttcataa aacttgaca gatgaactgg ctgccttaca 720		
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780		
aaatccaagt acaagtttg gaccactct ggaacctgag gaagtggtaa acaggctgat 840		
gcatggatt ctgactgagc agaagatgtat ttttattcca tcttctatag ctttttaac 900		
aacatggaa aggatccttc ctgagcgttt cctggcagtt taaaacgaa aaatcagtgt 960		
taagttgat gcagttattt gatataaaat gaaagcgaa taagcaccta gttttctgaa 1020		
aactgattta ccaggtttag gttgatgtca tctaatacgat ccagaatttt aatgtttgaa 1080		
cttctgtttt ttcttaattat ccccatttct tcaatatcat ttttgaggct ttggcagtct 1140		
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200		
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taatttccaa gattattttgt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320		
ttatttaaca tatatttttta ttgttgcattt cacttaaattt ttgtataattt ttgttgcattt 1380		
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gccactctgt tccctgagag atacccatcaca ttccaaatgcc aaacatttct gcacaggaa 1560		
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattt 1620		
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaa 1680		
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740		
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1771		
<210> 159		

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1														

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
		20					25						30		

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
		35				40						45			

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
		50				55					60				

Leu	Trp	Asp	Ile	Asn	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
		65			70			75					80	

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
		85				90						95			

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
		100				105						110			

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
		115			120							125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
		130			135				140						

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
		145			150			155				160			

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
		165				170						175			

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
		180			185							190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Gln	Ile	
		195			200				205						

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
		210			215					220					

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
		225			230			235				240			

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
		245			250			255							

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctgggttag tctatacacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgccgagccgc cgcccgccggc 60
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

attgttcgc tggcctgtt gatgcctggc ccctgtatg ggctgttcg ctccctatac 180
 agaagtgtt ccatgccacc taaggagac tcaaggacagc cattattct cacccttac 240
 attgaagctg ggaagatcca aaaaggaaga gaatttagt tggcggccc ttcccagga 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agactacaa cagcaacctc 360
 ttcttcgtt tcttcccagc tcagatacag ccagaagatg ccccaagtat tctctggcta 420
 cagggtggc cgggaggtt atccatgtt ggactcttt tggaacatgg gccttatgtt 480
 gtcacaagta acatgaccc tgcgtacaga gacttcccct ggaccacaac gctctccatg 540
 ctttacattg acaatccagt gggcacaggc ttcatgttta ctgtatgatac ccacggat 600
 gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660
 atatccctg aatataaaaa taatgactt tatgtcactg gggagtctt tgcagggaaa 720
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
 aacctgaacg gaattgctat tggagatgaa tatttctgatc ccgaatcaat tataggggc 840
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 aaaggatggg atccttatgt tggataaaact accttccca aagagaacat cagaggttt 1560
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaaa aattatctt 1620
 tcataatctgc aagattttt tcatcaataa aaattatcc tggaaacaagt gagctttgt 1680
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 ttaactaaa ggtgaaagg tatggatgt gtgacactga gacaagatgt ataaatgaaa 1800
 ttttagggtc ttgaatagga agtttaatt tcttctaaga gtaagtggaa agtgcagttg 1860
 taacaaacaa agctgtaca tcttttctg ccaataacag aagttggca tgccgtgaag 1920
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggtgaagct 1980
 ataatagttt tggggaaaag attctcaat gtataaagtc tttagaacaaa agaattctt 2040
 gaaataaaaaa tattatataa aaaagtaaaa aaaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgccca cctaaggagg actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgagggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 167
 agctctcaga ggctggcat aggg 24

<210> 168
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 168
 gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169
 <211> 2477
 <212> DNA
 <213> Homo sapiens

<400> 169
 cgagggtctt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
 atttttccct ttcttaacaa gttctaacag ctgttctaac agctagtat caggggtct 120
 tcttgctgga gaagaaaggc ctgagggcag agcagggcac tctcaactcg ggtgaccagc 180
 tccttgccctc tctgtggata acagagcatg agaaaagtgaa gagatgcagc ggagtggaggt 240
 gatggaaagtc taaaatagga aggaattttg ttttgcataat cagactctgg gacgttga 300
 cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
 ctgggctggg ataagacgtg ccggtaggat agggaaagact gggtttagtc ctaatatcaa 420
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 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaaa gcaagtattt 540
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 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
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 acatctgaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
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Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
 20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
 35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
 50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
 65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
 85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
 100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
 130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
 145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
 165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171
tggaaataccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
cttctgcctt ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173

ggactcactg gcccaggcct tcaatatcac cagccaggac gat

42

<210> 174

<211> 3106

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1683)

<223> a, t, c or g

<400> 174

aggctccgcg cgcggcgtga gtgcggactg gagtgggaac ccgggtcccc ggcgttagag 60
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 ggagggaccg cctgctgaag atgaaggcct gtggcttcaa caccctcacc acctatgttc 360
 cgtggAACCT gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
 aggccctcggt cctgatggcc gcagagatcg ggctgtgggt gatttcgtg ccaggcccct 480
 acatctgcag tgagatggac ctcggggct tgcccagctg gctactccaa gaccctggca 540
 tgaggctgag gacaacttac aagggttca cccaaagcgt ggacccctt tttgaccacc 600
 tggatgtccag ggtgggtgcca ctccagtaca agcgtgggg acctatcatt gccgtgcagg 660
 tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720
 cactggagga ccgtggcatt gtggaaactgc tcctgacttc agacaacaag gatggctga 780
 gcaaggggat tggccaggga gtctggcca ccatcaactt gcagtcaaca cacgagctgc 840
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 gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagccaaac acctggctt 3060
 ggctcaactgt cctgagttgc agtaaagcta taaccttcaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
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Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp
															30

Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln
															45

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe
															60

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp
															80

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr
															95

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
															110

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly
															125

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp
															140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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 ccctggtag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
 aaggggagca aagccggct cggcccaggc ccccccaggac ctccatctcc caatgttgg 180
 ggaatccgac acgtgacggt ctgtccggc ttcagacta gaggagcgct gtaaacgcca 240
 tggctcccaa gaagctgtcc tgccttcgtt cctctgtgtc gcccgtcagc ctgacgctac 300
 tgctgccccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctacttcgg gtaaccgcgg 420

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atgtgccctg gaactaccac gagccacagc ctggggtcta taacttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
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aaatttagccg ggcgtatgg tggcacctc taatccagg tacttgggag gctgaggc 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggtgt accactgcac 2460
tccagctgg ctgacagtqa qacactccat ctcaaaaaaa aaaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Ileu Leu Leu Pro Leu

1

5

10

15

Ser Leu Thr Leu Leu Leu Pro Glu Ala Asp Thr Arg Ser Phe Val Val

20

25

THE

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Glu Ala Pro Phe Arg Thr

25

40

PRO

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Thr Ala

50

55

419

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
560		
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatcc tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac cttaacctcc 50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gctttgaaca cgtctgcaag cccaaatgg agcatctgat tggttatgag gtatttgagt 60
gcacccacaa tatggcttaac atgttggaaaa agcttctcat cagttacata tccattatatt 120
gtgtttatgg ctttatctgc ctctacactc tcttctgggtt attcaggata ctttgaagg 180
aatattctt cggaaaaatgc agagaagaga gcaagttttag tgacattcca gatgtcaaaa 240
acgattttgc gttcccttctt cacatggtag accagttatga ccagctatat tccaagcgtt 300
ttggtgtgtt cttgtcagaa gtttagtggaaa ataaaacttag ggaaatttagt ttgaaccatg 360
agtggacatt tgaaaaactc aggccagcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcacatgtt catgtgtcg ggggtgccccg atgctgtctt tgacccatca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaga gctccacactc tgccactgccc ctgcaaaaatg tgaacagact gcttttagct 600
ttcttcgca tcaacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattccctg 660
cctgggtgtt tttgtcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcgccacctt aagattctcc 780
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
caaagtttagt cattcataat gacggcaacta aactcttggt actgaacagc cttaaagaaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
ttttcagctt ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
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aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140
ctaacaacaa gctcgaatcc ttaccagtgg cagtttttag tttacagaaaa ctcagatgct 1200
tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
tgcagcatt gcatatcact gggaaacaaag tggacattct gccaaacaaat ttgtttaat 1320

gcataaaagt	gaggactttg	aatctggac	agaactgcat	cacctca	tc	ccagagaaa	1380	
ttggtcagct	ctccccagctc	actcagctgg	agctgaaggg	gaactgctt	gaccgc	ctgc	1440	
cagcccgagct	ggggccagtg	cgatgctca	agaaaagcg	gcttgg	ttgt	gaagatcacc	1500	
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ttgcaatgg	gatttaaact	aagataat	atgcacagt	atgtgcag	gga	acaactt	cct	1620
agattgcaag	tgctcacgta	caagttat	caagataat	cattttag	gga	gtagata	cat	1680
cttttaaaat	aaaacagaga	ggatgcata	aaggctgata	gaagacata	aa	ctgaatgt	tc	1740
aatgtttgt	gggttttaag	tcattcatt	ccaaatcatt	ttttttt	tc	tttggggaa	1800	
agggaaaggaa	aaattataat	cactaatctt	ggttctttt	aaattgtt	tg	taacttggat	1860	
gctggccgcta	ctgaatgtt	acaaattgct	tgcctgctaa	agtaaaat	gtat	taaattgaca	1920	
ttttcttact	aaaaaaaaaa	aaaaaaaa					1947	

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
 20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
 35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
50 55 60

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
65				70						75					80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
 180 185 190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187

gaccaacttt ctctgggagt gagg

24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60
actttttta tttttttt tccatctctg ggccagctg ggatcctagg ccgccttggg 120
aagacatttgc tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
 gcacttatct gcctaggtac atcqaagtct tttgacctcc atacagtat tatgcctgtc 300
 atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcttac 360
 ttcaaaatac acaaacgcgc aaaaagctgca aaggaacctg aagctgtggc tggaaaaat 420
 cacaaccagg acaagggtgtg gtggggcaag aacagccagg cccaaaccat tgccacggag 480
 tcttgcctg cctgcagtg ctgtgaagga tatagaatgt gtgcacgttt tgattccctg 540
 ccaccttgct gttgcgacat aaatgagggc ctctgagttt ggaaaggctc ctttctcaa 600
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tggttgat gtgcaggcac 660
 agaagaaagg cacagctccc catcagttc atggaaaata actcagtgcc tgctggaaac 720
 cagctgctgg agatccctac agagagcttc cactggggc aacccttcca ggaaggagtt 780
 ggggagagag aaccctact gtggggatg ctgataaacc agtcacacag ctgctctatt 840
 ctcacacaaa tctaccctt gcgtgctgg aactgacgtt tccctggagg tggccagaaa 900
 gctgatgtaa cacagagccat ataaaagctg tcggctcta aggctgccc ggccttgcc 960
 aaaatggagc ttgtaaagaag gtcatgcca ttgaccctt taattctctc ctgtttggcg 1020
 gagctgacaa tggcgaggc tgaaggcaat gcaagctgca cagtcagttt agggggtgcc 1080
 aatatggcgag agacccacaaa agccatgatc ctgcaactca atcccaagtga gaactgcacc 1140
 tggacaataa aagagaccaga aaacaaaagc atcagaattt tctttccta tggccagctt 1200
 gatccagatg gaagctgtga aagtggaaac attaaagttt ttgacggaaac ctccagcaat 1260
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttccctgtatt tgaatcatca 1320
 tccagtagat tgacgtttca aatagttact gactcagcaa gaattcaag aactgtctt 1380
 gtcttctact acttcttctc tcttaacatc tctattccaa actgtggcg ttacctggat 1440
 accttggaaag gatccttcac cagcccaat taccggaaac cgcattctga gctggcttat 1500
 tgggtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560
 ttcctagaaa tagacaaaca gtgcaattt gatttcttg ccatctatga tggcccttcc 1620
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 gcttcctaca cctcaattt tgcagaaaac atcaacacta catcttaac ttgctcttct 1800
 gacaggatga gagttattat aagcaatcc tacctagagg cttaactc taatggaaat 1860
 aacttgcac taaaagaccc aacttgcaga cccaaattat caaatgttgc ggaattttct 1920
 gtccttta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
 aatataatca cctttctgc atcctcaact tctgaagtga tcaccgtca gaaacaactc 2040
 cagattattt tgaagtgtga aatggacat aattctacag tggagataat atacataaca 2100
 gaagatgtg taatacataa tcaaatgca ctggggcaat ataacaccag catggcttctt 2160
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220
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 gatacctgta gagcctctcc cacctctgac tttgcatttc caacctacga cctaatacaag 2340
 agtggatgtg gtcgagatga aacttgcata gttatccct tattggaca ctatgggaga 2400
 ttccagttt atgcctttaa attcttgcata agttagatgt ctgtgtatct gcagtgtaaa 2460
 gtttgatgtat gtgatagcag tgaccaccag tctcgctgca atcaagggtt ggtgtccaga 2520
 agcaaaacgag acatttctt atataaatgg aaaacagatt ccattatagg acccattcgt 2580
 ctgaaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640
 gaaactccaa accagcctt caacagtgtg catctgttt ctttcatggt tctagcttg 2700
 aatgtgtgaa ctgttagcgc aatcacatg aggcatggg taaatcaacg ggcagactac 2760
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgttcc 2820
 tccagatgc caaaggaaat gctacctcggt ggctacacat attatgaata aatgagggaa 2880
 ggcctgaaag tgacacacag gcctgcatgt aaaaaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe		
580	585	590

595	600	605
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr		

<210> 191
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 191
 tctctattcc aaactgtggc g

21

<210> 192
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 192
 tttgatgacg attcgaaggt gg

22

<210> 193
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 193
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgac

47

<210> 194
 <211> 2362
 <212> DNA
 <213> Homo sapiens

<400> 194
 gacggaagaa cagcgatccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
 cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgct gttgctgtg 120
 ctgctgctgc cggccggccgtgac cacagcgcca cgcgcgttca cccccacctgg 180

gagtccctgg acgcccggca gctgcccgcg tggtttgcacc aggccaagtt cggcatcttc 240
 atccactggg gagtgtttc cgtgcccagc ttccgttagcg agtggttctg gtggatttgg 300
 caaaaaggaaa agataccgaa gtagtggaa ttatgaaag ataattaccc tcctagttc 360
 aaatatgaag atttggacc actattaca gcaaaaatttt ttaatgc当地 ccagtggca 420
 gatattttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
 tttaccttgc ggggtcaga atatcgtgg aactgaaatg ccatagatga gggggcccaag 540
 agggacattt tcaaggaact tgaggttagcc attaggaaca gaactgaccc ggggttttgg 600
 ctgtactatt cccttttga atggttcat ccgcctttcc ttgaggatga atccagttca 660
 ttccataaggc ggcaatttcc agttctaaag acattgcccag agctctatga gttagtgaac 720
 aactatcagc ctgaggttct gtggtcggat ggtgacggag gggccggca tcaatactgg 780
 aacagcacag gttcttggc ctggttatataatgaaagcc cagttcgcccc cacagtagtc 840
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
 gatcggtata acccaggaca tcttttgc当地 catabatggg aaaactgc当地 gacaatagac 960
 aaactgtcctt ggggtatag gaggaaagct ggaatctctg actatcttac aattgaagaa 1020
 ttgggtgaagc aactttaga gacagttca tggtaggaa atctttgtat gaatatttggg 1080
 cccacactat atggcaccat ttctgttagtt tttgaggagc gactgaggca agtgggggtcc 1140
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 taaactcatt gtgcaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaaagt tgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198
 aacttgca
 gtc atc
 aagccact
 ctgc

24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199
 ttccgtgccc
 agcttcggta
 gcgagtggtt
 ctgggttat
 tggca

45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
 agcaggaaaa
 tccggatgtc
 tcggtatga
 agtggagcag
 tgagtgtgag
 cctcaacata

60
 gttccagaac
 tctccatccg
 gactagttat
 tgagcatctg
 cctctcatat
 caccagtgc

120
 catctgaggt
 gttccctgg
 ctctgaaggg
 gttaggcacga
 tggccaggtg
 cttcagccctg

180
 gtgttgcctc
 tcacttccat
 ctggaccacg
 aggctcctgg
 tccaaggctc
 tttgcgtgca

240
 gaagagctt
 ccatccaggt
 gtcatgcaga
 attatgggg
 tcacccttgt
 gagcaaaaaag

300
 gcgaaccacg
 agctgaattt
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 aaggaggcct
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 gggactaagt

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 gctttgaaaac
 ttgcagctat

420
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 gagatggatt
 cgtggtcatt
 tctaggatta
 gcccggggcc
 caagtgtgg

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 aaaaaatgggg
 tgggtgtct
 gatttggaaag
 gttccagtga
 gccgacagtt
 tgcagccctat

540
 tggtaacaact
 catctgataac
 ttggactaac
 tctgtcattc
 cagaaattat
 caccaccaaa

600
 gatccccat
 tcaacactca
 aactgcaaca
 caaacaacag
 aatttattgt
 cagtgacagt

660
 acctactcg
 tggcatcccc
 ttactctaca
 atacctgcc
 ctactactac
 tccctctgct

720
 ccagcttcca
 ctcttattcc
 acggagaaaa
 aaattgattt
 gtgtcacaga
 agtttttatg

780
 gaaactagca
 ccatgtctac
 agaaaactgaa
 ccatttgg
 aaaataaagc
 agcattcaag

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 ggtatgtgaa
 ggccttcct

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 gaaggaaaatg
 atcgaaacca
 aagttagaaa
 ggaggagaag

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 gcaaccctaa
 tgaggaatca
 aagaaaactg
 ataaaaaacc
 agaagagtcc

1080
 aagagtccaa
 gcaaaaactac
 cgtgcgatgc
 ctggaaagctg
 aagtttagat
 gagacagaaa

1140
 tgaggagaca
 cacctgaggg
 tggtttctt
 catgctcctt
 accctgcccc
 agctggggaa

1200
 atcaaaaagg
 ccaaagaacc
 aaagaagaaa
 gtccaccctt
 ggttccctaac
 tggaaatcagc

1260
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 cattggacta
 tggagtgac
 caaagagaat
 gcccctctcc
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1320
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 agcttccac
 ggccttcata
 gcctggctat

1380
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 tatcccactg
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 gtttgcaaaa
 gtgcaaggac
 ctaaaacatc

1440

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg gttgaaagc 1500
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 gcaggactg taaacacaga cagggtcaaa gtgtttctc tgaacacatt gagttggaa 1800
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 aggaaatata ctttacaag taacaaaaat aaaaactctt ataaatttctt attttatct 1920
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 gactaatctt attcattttc tctaataatgg caaccattat aacctaattt tattattaac 2220
 atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaaatatt 2340
 tgtgacaaaa aattaaagca ttttagaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr
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Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
															30
20								25							

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
															45
35								40							

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
															60
50								55							

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
															80
65								70			75				

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
															95
85									90						

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
															110
100									105						

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
															125
115								120							

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
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130								135							

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 202
 gagctttcca tccaggtgtc atgc

24

<210> 203
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 203		
gtcagtgaca gtacctactc gg		22
<210> 204		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 204		
tggagcagga ggagtagtag tagg		24
<210> 205		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 205		
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt		50
<210> 206		
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<212> DNA		
<213> Homo sapiens		
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<221> modified_base		
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<223> a, t, c or g		
<220>		
<221> modified_base		
<222> (977)		
<223> a, t, c or g		
<220>		
<221> modified_base		
<222> (996)		
<223> a, t, c or g		
<220>		
<221> modified_base		

<222> (1003)

<223> a, t, c or g

<400> 206

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 ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgta 120
 gaaaaactgcc gcccgtctgc cacggctctgc ccacccaacg cgaagacggt aaccgcgttg 180
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 accgcagatc catcaactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
 ccaacacaat tctttcttc cgcttggata ttgcgtatggg cctactttac atcacactct 360
 gcatagtggtt cctgatgacg tgcaaaacccc ccctatataat gggccctgag tatatcaagt 420
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20

25

30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35

40

45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50

55

60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65

70

75

80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 208
 gcttggatat tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattatgtga ggaactagaa cgggacaaga gggtaacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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 cccattgtctc ctgtcgcccg gctcctacgg actgcccttc tacaacggct tctactactc 180
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacactcc ttaatggagt 240
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125	
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr			
130	135	140	
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu			
145	150	155	160
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg			
165	170	175	
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala			
180	185	190	
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly			
195	200	205	
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr			
210	215	220	
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro			
225	230	235	240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp			
245	250	255	
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu			
260	265	270	
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu			
275	280	285	
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys			
290	295	300	
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser			
305	310	315	320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu			
325	330	335	
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr			
340	345	350	
Gly Val Tyr Cys Tyr Arg Gln His			
355	360		

<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence
<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

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18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcccttgtg gtttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaatgct

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 219
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<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 tggccagggg agggtgcacc aggeggcccc cctgagcgcac gctccccatg atgacgccc 180
 cgggaacttc cagtacgacc atgaggttt cctgggacgg gaagtggcca aggaattcga 240
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 cagctccaaa tctgagccctc caccacatag actgaaaactc ccctggcccc agccctctcc 1380
 tgcctggcct ggctgggac acctcctctc tgccaggagg caataaaaagc cagcggcggg 1440
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 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
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Lys	Pro	Ser	Pro
20	25	30	
Asp	Ala	Gly	Pro
His	Pro	Gly	Gln
Arg	Val	His	Gly
35	30	35	40
Ala	Ala	Pro	Asp
Leu	Ser	Ala	Pro
40	45	40	45
His	Gly	Asn	Phe
Gln	Tyr	Asp	His
50	55	50	55
Glu	Ala	Phe	Leu
Arg	Val	Gly	Gly
60	65	60	65
Asp	Gln	Asp	Glu
Glu	Leu	Glu	Ser
70	75	70	75
Thr	Pro	Glu	Gln
80	85	80	85
Ala	Arg	Ala	Arg
Leu	Leu	Leu	Leu
Gly	Arg	Val	Asp
95	85	90	95
Asp	Arg	Asp	Gly
Arg	Ile	Val	Asp
100	115	100	115
Asp	Arg	Asp	Gly
Ala	Ile	Val	Asp
Trp	Arg	Asp	Gly
110	125	110	125
His	Ile	Arg	Asp
Ser	Val	Ser	Val
125	130	125	130
Ala	Ala	Trp	Asp
Trp	Asp	Thr	Tyr
130	135	130	135
Asp	Arg	Asp	Arg
Arg	Val	Gly	Trp
140	145	140	145
Glu	Glu	Glu	Glu
Leu	Leu	Leu	Leu
Arg	Arg	Arg	Arg
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
145	150	145	150
Asp	Gly	Asp	Gly
Ala	Tyr	Ala	Tyr
155	160	155	160
Glu	Asp	Glu	Asp
Asp	Val	Asp	Val
160	165	160	165
Arg	Arg	Arg	Arg
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
165	170	165	170
Asp	Gly	Asp	Gly
Ala	Tyr	Ala	Tyr
175	180	175	180
Asp	Gly	Asp	Gly
Ser	Val	Ser	Val
180	185	180	185
Met	Ala	Thr	Arg
Ala	Arg	Arg	Arg
185	190	185	190
Asp	Glu	Asp	Glu
Asp	Asp	Asp	Asp
190	195	190	195
Arg	Arg	Arg	Arg
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
195	200	195	200
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
205	210	205	210
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
210	215	210	215
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
220	225	220	225
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
225	230	225	230
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
230	235	230	235
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
235	240	235	240
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
240	245	240	245
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
245	250	245	250
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
250	255	250	255
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
255	260	255	260
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
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Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
265	270	265	270
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
270	275	270	275
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
275	280	275	280
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
280	285	280	285
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
285	290	285	290
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
290	295	290	295
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
295	300	295	300
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
300	305	300	305
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
305	310	305	310
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
310	315	310	315
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
315	320	315	320
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
320	325	320	325
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
325	330	325	330
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
330	335	330	335
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
335	340	335	340
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
340	345	340	345
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
345	350	345	350
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
350	355	350	355
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
355	360	355	360
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
360	365	360	365
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
365	370	365	370
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
370	375	370	375
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
375	380	375	380
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
380	385	380	385
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
385	390	385	390
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
390	395	390	395
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
395	400	395	400
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
400	405	400	405
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
405	410	405	410
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
410	415	410	415
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
415	420	415	420
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
420	425	420	425
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
425	430	425	430
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
430	435	430	435
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
435	440	435	440
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
440	445	440	445
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
445	450	445	450
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
450	455	450	455
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
455	460	455	460
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
460	465	460	465
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
465	470	465	470
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
470	475	470	475
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
475	480	475	480
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
480	485	480	485
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
485	490	485	490
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
490	495	490	495
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr	Asp	Gly
495	500	495	500
Asp	Gly	Asp	Gly
Leu	Val	Ile	Ile
Asp	Asp	Ala	Ala
500	505	500	505
Arg	Asn	Asn	Asn
Asn	Asn	Asn	Asn
Ala	Ala	Ala	Ala
Thr	Tyr		

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcgtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44

 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

 <400> 226
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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
			20				25					30			

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
	35					40				45					

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
	50					55				60					

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
	65					70			75				80		

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
	85							90				95			

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
	100						105				110				

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
	115						120			125					

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
	130					135				140					

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
	145				150				155			160			

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
	165					170				175					

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
	180						185				190				

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
	195					200				205					

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
	210					215				220					

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
	225				230			235			240				

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
	245						250			255					

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgccc 18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc 18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc 24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234
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<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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 gtcggggcgcc cggctgcggg cgcaagacgg agatgcacgg gcttggggcc accctgtgt 180
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aaaaaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

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<223> Synthetic oligonucleotide probe		
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<400> 238		49
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<210> 239		
<211> 24		
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<400> 239		24
gcagagcgga gatgcagcggtt		
<210> 240		
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<223> Synthetic Oligonucleotide Probe		
<400> 240		18
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<400> 241		18
cctggcaaa aatgcaac		

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc 24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 cacacataca ctttcctctc cttcaactgaa gactcacagt cactcactct 200
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 aataaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
														45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
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Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
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Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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140														

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 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
 185 190 195
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
 200 205 210
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 215 220 225
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
 245 250 255
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
 260 265 270
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
 275 280 285
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
 290 295 300
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
 305 310 315
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
 320 325 330
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
 380 385 390
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
 395 400 405
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
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425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
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 Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
 695 700 705
 Leu Pro Pro Leu Ser Gln Asn Ser
 710

<210> 246
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 246
 aacaaggtaa gatgccatcc tg 22

<210> 247
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 247
 aaacttgtcg atggagacca gctc 24

<210> 248
 <211> 45
 <212> DNA
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<220>
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<400> 248
 aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249
 <211> 3401
 <212> DNA
 <213> Homo Sapien

<400> 249
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 <213> Homo Sapien
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 20 25 30
 Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg
 35 40 45
 Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
 50 55 60
 Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
 65 70 75
 Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu
 80 85 90
 Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

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Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385				390	
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400				405	
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415				420	
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430				435	
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
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Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460				465	
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475				480	
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490				495	
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505				510	
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
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Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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<400> 251

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<210> 253
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<210> 254
<211> 1650
<212> DNA
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<211> 452

<212> PRT

<213> Homo Sapien

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20

25

30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val

35

40

45

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Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln		
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Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu		
80	85	90
Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp		
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Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr		
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Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu		
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Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe		
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Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu		
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230	235	240
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275	280	285
Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His		
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Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly		

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
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Gln Glu		
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 35 40 45
 Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
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 Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
 65 70 75
 Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
 80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
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 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
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<212> PRT

<213> Homo Sapien

<400> 259

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														15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu	545	550	555

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

ggcgcgcgct ctctcccgcc gccccacacct gtctgagcgg cgcaagcggc 50

cgcgccccgg gcgggctgct cggcgccgaa cagtgctcggt catggcaggg 100

atcccagggc tcctcttcct tctttttt ctgctctgtg ctgttggca 150

agtgagccct tacagtgc cctggaaacc cacttggcct gcataaccgc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250

ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300

taaggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350

atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400

tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450

ttcagggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500

tcagcatttt tgggaaggac ttccctgctca actaccctt ctcaacatca 550

gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600

cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650

cccagaagct tcgagtgggc ttccctaaagc ccaagttaa agatgggtgg 700

cgagggggcca acgactccac ttccagccatg cccgagcaga taaaatttca 750

gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggcga 800

atgccaatga catcgccatg gattatgatt atgccttcct ggaactcaaa 850

aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900

gcagctgcca gggggcagaa ttccatttc tggttatgac aatgaccgac 950

caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000

ttgctctacc agcaatgcga tgcccagcca gggggccagcg ggtctgggt 1050

ctatgtgagg atgtggaaga gacagcagca gaagtggag cgaaaaatta 1100

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 gatttcaacg tggctgtcag aatcaactcct ctc当地atatg cccagatttg 1200
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 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550
 caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600
 atatttggca tacaagagat atgaaaaaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu
1				5					10				15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
					20				25					30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
						35			40					45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
					50				55				60	

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65				70						75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
					80				85					90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
									95					105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
					110				115					120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
 380

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
 gcatgcacct gggtctctcg agcctgctgc ctgctcccc gccccaccag 50
 ccatggtgtt ttctggaggcg ccccccagccc tgggtggggg ctgtctcgcc 100
 accttcacct ccctgctgt gctggcgtcg acagccatcc tcaatgcggc 150
 caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200
 ttgtggcgg cgaggacaga actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccga ccactgcgca ggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
 cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgct 500
 ccatacagtt ctcagagcgg gtcctgcca tctgcctacc tgatgcctct 550
 atccacacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
 ggacagggac ccatcactga ggacatgctg tgtgccgct acttggaggg 750
 ggagcgggat gttgtctgg gcgactccgg gggcccccctc atgtgccagg 800
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900
 ctgggtggag aagatcgtgc aagggtgtca gtcggcgggg cgcgctcagg 950
 ggggtggggc ctcaggcga ccgagccagg gtcctggggc cgccgcgcgc 1000
 tcctaggcgc cagcggcgcg cggggctcgg atctgaaagg cggccagatc 1050
 cacatctgga tctggatctg cggcggcctc gggcggttcc ccccgccgta 1100
 aataggcgtca tctacacctta cctctggggg cccggacggc tgctgcggaa 1150

aggaaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc cggccccac gacttccggc 1250
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
 ataggtatcc gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
 ataaattatt tattctccaa aaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Cys	Leu	
1				5					10				15	
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20					25				30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40				45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55					60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65				70					75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80				85					90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95				100					105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110				115					120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125				130					135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140				145					150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155				160					165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170				175					180	

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 190 195
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 295 300
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
 305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagagggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
gggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
ggcaggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gctccataca gttcccttgc cccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggagggggaa gcggggatgct tgtctggcg actccggggg ccccccattg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcgaaagtct 50

gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggggagct gcacaacctc taccgggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgact tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
 caaggagcgc ggggcccgcg gcgagaatct gttcgccatc acagacgagg 300
 gcatggacgt gcccgtggcc atggaggagt ggcaccacga gcgtgagcac 350
 tacaacctca gcgcgcacac ctgcagccca ggccagatgt gcggccacta 400
 cacgcagggtg gatatggcca agacagagag gatcggctgt gttccact 450
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
 tctgtgaacc catcggaagc ccggaaagatg ctcaggattt gccttacctg 650
 gtaactgagg ccccatcctt ccggcgact gaagcatcag actctaggaa 700
 aatgggtact cttttccc tagcaacggg gattccggct ttcttggtaa 750
 cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
 caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850
 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900
 gcctgcctc cttggatgag gagccagttt cttcccttca atcgacccat 950
 gttccatatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
 ctcttaggac ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
 caaggaaact cttcccttca gcccaggagg aggctgaggg tgaggctgag 1100
 ttgcctcctt ccagtgaggt cttggcctca gttttccag cccaggacaa 1150
 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
 agtcctgccc caatttcccc aatacctctg ccacccgctaa tgccacgggt 1250
 gggcggtccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300
 caagccttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350
 gcccctctactt gggactactg ctcctgcctc ctctgggttt ggctggaatc 1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
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 ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagtcagga ggccgcctga 1600
 ggactgcaca cggggccac acctctcctg cccctccctc ctgagtcctg 1650
 ggggtggag gatttggagg agctcactgc ctacctggcc tggggctgtc 1700
 tgcccacaca gcatgtgcgc tctcctgag tgcctgtgta gctggggatg 1750
 gggattccta gggcagatg aaggacaagc cccactggag tggggtttt 1800
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 ataaaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1									10					15

Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
									25					30

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
									35					45

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
									50		55			60

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
									65		70			75

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
									80		85			90

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
									95		100			105

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
									110		115			120

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
									125		130			135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
 140 145 150
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
 155 160 165
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
 200 205 210
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420
 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435
 Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
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 Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
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 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

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 <211> 24
 <212> DNA
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<220>
 <223> Synthetic Oligonucleotide Probe

<400> 287
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<210> 288
 <211> 45
 <212> DNA
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<220>
 <223> Synthetic Oligonucleotide Probe

<400> 288
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<210> 289
 <211> 3662
 <212> DNA
 <213> Homo Sapien

<400> 289
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 caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200
 acaacaatga attggagacc attccaaatc tggaccagt ctggcaaat 250
 attacacttc tctccttggc tggaaacagg attgttggaaa tactccctga 300
 acatctgaaa gagtttcagt ccctgaaac ttggaccctt agcagcaaca 350
 atattcaga gctccaaact gcattccag ccctacagct caaatatctg 400
 tatctcaaca gcaaccgagt cacatcaatg gaacctgggt atttgacaa 450
 ttggccaac acactccttg tggtaaagct gaacaggaac cgaatctcag 500
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 aaccgaaaca agattaaaaa tggatgtgg ctgacattcc aaggcattgg 600
 tgctctgaag tctctgaaaa tgcaaaagaaa tggagtaacg aaacttatgg 650
 atggagctt ttggggctg agcaacatgg aaatttgca gctggaccat 700
 aacaaccaa cagagattac caaaggctgg cttaacggct tgctgtatgc 750
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 gcatttaat acatcaagcc ttttgctgca ttgcccagctt aatggctcc 1250
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tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
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<210> 290
 <211> 1059
 <212> PRT
 <213> Homo Sapien

<400> 290
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 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
 20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 35 40 45
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
 155 160 165
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
 170 175 180
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
 185 190 195
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
 200 205 210
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
 215 220 225
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
 230 235 240
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
 245 250 255
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
 260 265 270
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
 275 280 285
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

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 575 580 585
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 590 595 600
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 605 610 615
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 620 625 630
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 635 640 645
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 650 655 660
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 665 670 675
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 680 685 690
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 695 700 705
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 710 715 720
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 725 730 735
 Thr Ala Pro Ser Leu Asp Asp Gly Trp Ala Thr Val Gly Val
 740 745 750
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
 1025 1030 1035
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
 1040 1045 1050
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
 1055
 <210> 291
 <211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
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gatatttttgaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

	155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly			
170	175	180	
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly			
185	190	195	
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg			
200	205	210	
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp			
215	220	225	
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln			
230	235	240	
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile			
245	250	255	
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val			
260	265	270	
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp			
275	280	285	
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His			
290	295	300	
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp			
305	310	315	
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys			
320	325	330	
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp			
335	340	345	
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro			
350	355	360	
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys			
365	370	375	
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn			
380	385	390	
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val			
395	400	405	
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp			
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 440 445 450
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
 470 475 480
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
 485 490 495
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
 500 505 510
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
 515 520 525
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
 530 535 540
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
 545 550 555
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
 560 565 570
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn
 605 610 615
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
 620 625 630
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<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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 cgggcagccc tctgggttag ccgcccggcg cccatgcccc actacactgcc 400
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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
 35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
 50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
 65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
 80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
 485 490 495
 Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
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 Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
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 Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
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 Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
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 Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
 560 565 570
 Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
 575 580 585
 His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
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 Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
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 Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
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 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 635 640 645
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 650 655 660
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 665 670 675
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 680 685 690
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 695 700 705
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 710 715 720
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 740 745 750

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 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 800 805 810
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
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 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys
 830 835 840
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 935 940 945
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 950 955 960
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 965 970 975
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 980 985 990
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 995 1000 1005
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Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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<400> 296
cctaaactga actggacca 19

<210> 297
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ggctggagac actgaacct 19

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<400> 300
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<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

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<210> 312
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<220>
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<400> 312
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<210> 313
 <211> 45
 <212> DNA
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<220>
 <223> Synthetic Oligonucleotide Probe

<400> 313
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<210> 314
 <211> 3003
 <212> DNA
 <213> Homo Sapien

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<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu
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Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val
				20					25					30
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys
					35				40					45
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys
				50					55					60
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys
				65					70					75
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu
				80					85					90
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met
									95					105
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met
				110					115					120
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met
				125					130					135
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg
				140					145					150
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg
				155					160					165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 316
 gatggttcct gctcaagtgc cctg 24

<210> 317
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 317
 ttgcacttgtt aggacccacg tacg 24

<210> 318
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 318
 ctgatgggag gacctgtgt aatgtgctac aggaagagcc 50

<210> 319
 <211> 2110
 <212> DNA

<213> Homo Sapien

<400> 319

cttccttgaa aaggattatc acctgatcag gttctctctg catttgc 50
tttagattgt gaaaatgtggc tcaaggcttt cacaacttc ctttccttg 100
caacaggtgc ttgctcgaaa ctgaaggta cagtgccatc acacactgtc 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
caactccagca tcagacatcc agatcatatg gctattttag agacccca 250
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 ttcaaggaa agatggattc aaataaatta ttctgtttt gctttaaaa 2100
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
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Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20				25				30		

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35				40				45		

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50				55				60		

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

<210> 321
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 321
 gatccctgtca caaagccagt ggtgc 25

<210> 322
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 322
 cactgacagg gttcctcacc cagg 24

<210> 323
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccggaggt cttgcaggta ccctggcagt 50

cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggcgc cctgcttgc aaaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggtaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtg 300

ataactgctc ttccctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400

aagagtggaa gagtattgag cccgtttcat catggtttg tccaggttct 450

gttctgtatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcc 550

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ctctgtatga tatttgcattt gcaactctgt tttccggact gttatttagga 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750

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gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

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aaaccttctt aaccacttca tttaagctga aaaaaaaaaa aaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val

1 5 10 15

Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215	220	225
-----	-----	-----

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
 230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
 245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
 260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
 275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
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 gtttagctgtc tagcgcttag caaggtgcct ttgtacctca ggtgttttag 2050
 gtgtgagatg tttcagtgaa ccaaagttct gataccttgt ttacatgttt 2100

gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150
 cctaccagaa aaaaaaaaa 2168

<210> 332
 <211> 533
 <212> PRT
 <213> Homo Sapien

<400> 332
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 Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met
 20 25 30
 Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
 35 40 45
 Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
 50 55 60
 Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
 65 70 75
 Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
 80 85 90
 Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
 95 100 105
 Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
 110 115 120
 Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
 125 130 135
 Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
 140 145 150
 Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
 155 160 165
 Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
 170 175 180
 Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
 185 190 195
 Leu Asp Ala Gly Glu Ala Thr Thr Lys Ser Gln Val Leu
 200 205 210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
 215 220 225
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
 245 250 255
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
 260 265 270
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
 275 280 285
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
 290 295 300
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
 305 310 315
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
 320 325 330
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
 335 340 345
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
 350 355 360
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
 365 370 375
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
 380 385 390
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
 395 400 405
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
 410 415 420
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
 425 430 435
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
 440 445 450
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
 455 460 465
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

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<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
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<220>
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<400> 337
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<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

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agacaggaca atcttcttgg ggatgctggc cctggaaagcc agcgggcatt 200
gctctgtctt tggcctcatt gaccccaatgt tctctggta aaactgaaag 250
cctactactg gcctggtgcc catcaatcca ttgatccttgc aggtgtgcc 300
cctggggcac ccacccatggca gggccatcca ccatgcgact gagtccttg 350
ttggctctgc tgcggccagc gcttcccttc atcttagggc tgtctctggg 400
gtgcagccctg agcctccctgc gggttccctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgta ggggagcgcag gaggccaca gaatccagat 500
tcgagagctc ggcttagacca aagtgtatgaa gacttcaaac ccggattgt 550
ccccctactac agggacccca acaaggccata caagaagggtg ctcaggactc 600
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 cccgttggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450
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 caccctgttgc ttggcttacg ggccacgaga aggtggccgt ggagctccag 1950
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 cctggacga ggctggcctg gtcgcgtgt cgagcagagg cccctccca 2050
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tttccttac caccgtgtgg acaaggcctg ggcccgaaatg cctcaaccgc 2150
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 gcccgcctgg gggccctaac ctcattacct ttcccttgtc tgcctcagcc 2700
 ccaggaaggg caaggcaaga tggtgacag atagagaatt gttgctgtat 2750
 ttttaata taaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
									20				30	

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
									35				45	

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
									50				60	

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
									65				75	

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
									80				90	

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
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95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
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 <211> 1572
 <212> DNA
 <213> Homo Sapien

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 cttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
 ggtatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500
 ttccttgcac gccccactac gtttgcatac attgaaaacc taaagtattt 550
 tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaatgt 700
 tcctgaacag ggagggatga tttgaagat atctgaagat aaacagctag 750
 cagtttgcct gaaatatgct ggagtatttgc cagaaaatgc agaagatgct 800
 gatggaaaag atgtatttaa taccaaattct gttggcctt ctattaaaga 850
 ggcaatgact tattcacccca accaggtgt agaaggctgt tgtagata 900
 tggctgttac ttttatgga ctgactccaa atcagatgca tgtgtatgt 950
 tatgggtat accgccttag ggcatttggg catattttca atgatgcatt 1000
 gttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
 agcgtgaata tgatcttgtt ataggacgtg tgtagtgcatt attttagta 1100
 gtaactacat atccaaataca gctgtatgtt tcttttctt ttctaatgg 1150
 gtggcactgg tataaccaca cattaaatgc agtagtacat ttttaatga 1200
 gggtggtttt tttttttaaa acacatgaac attgtaaatg tgtaggaaag 1250
 aagtgtttta agaataataa ttttgcataat aaactattaa taaatattat 1300
 atgtgataaa ttctaaatata tgaacattttt ggcacatattt 1350
 tttgctgatt gttttttttt ttttaacagg tcttttagcgt tctaaatgtt 1400
 gcaaatgata tctctagttg tgaatttgcgtt attaaatgtt aacttttagc 1450
 tgtgtgttcc cttaacttct aatactgatt tatgttctaa gcctcccaa 1500
 gttccaaatgg atttgccttc tcaaaatgtt caactaagca actaaagaaa 1550
 attaaatgtt aagttgaaaaa at 1572

<210> 341
 <211> 318
 <212> PRT
 <213> Homo Sapien

<400> 341

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								20			25			30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
								35			40			45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
								50			55			60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
								65			70			75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
								80			85			90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
								95			100			105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
								110			115			120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
								125			130			135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
								140			145			150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
								155			160			165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
								170			175			180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
								185			190			195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
								200			205			210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
								215			220			225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
								230			235			240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
								245			250			255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 342
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<210> 343
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 343
ctgggttcttc ctgcacg 18

<210> 344
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 344
gcccaaatgc cctaaggcg 28

<210> 345
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta ccggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaat acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349
ctatcaaatt aaccctcact aaaggatgt cttccatgcc aacccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaat acgactcact atagggcggc gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaagggacga ggaagatggg cgatgg 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
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<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcact atagggcttg ctgcggttt tgttcctg 48

<210> 355
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaaggagct gccgatccca ctggatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 356
ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaaggagcc cggcatggg ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
ctatgaaatt aaccctcact aaaggagcc aggcacaaa cggaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
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<220>
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<210> 362
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<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
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Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50				55				60		
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser		
				65				70				75		
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80				85				90		
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95				100				105		
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110				115				120		
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125				130				135		
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140				145				150		
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155				160				165		
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170				175				180		

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

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200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
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tgccagctgc atgctgccag tt 22

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cagaaggatg tcccggtggaa 20

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<400> 391
gccgctgtcc actgcag 17

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<210> 393

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<210> 394

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ccagggagac tggcgatg 18

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<400> 402
ggcagagact tccagtcact ga 22

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<400> 403
gccaagggtg gtgttagata gg 22

<210> 404
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<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
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<400> 405
gggacgtgct tctacaagaa cag 23

<210> 406
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<400> 406
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<210> 407
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<400> 407
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<400> 410

gccaggcctc acattcgt 18

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<400> 411
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<210> 412
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<400> 412
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 <210> 422
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 <212> PRT
 <213> Homo Sapien

<400> 423

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35				40				45		

Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55				60		

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
				65				70				75		

Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80				85				90		

Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95					100				105	

Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
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Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
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Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
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His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
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Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310